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(54) Title: MATERIALS AND METHODS RELATING TO IMPROVED VACCINATION STRATEGIES

(57) Abstract: The invention provides novel vaccination strategies based on a prime-boost vaccination regimen. The inventors have determined improved ways of boosting an immune response in a patient previously primed or exposed to a plurality of epitopes. The improved method requires the epitopes in the boosting phase to be administered individually, i.e. held on separate peptide constructs.

MATERIALS AND METHODS RELATING TO IMPROVED VACCINATION STRATEGIES

The present invention relates to materials and methods for improving vaccination strategies. Particularly, but not exclusively, the invention relates to "prime-boost" vaccination protocols in which the immune system is induced by a priming composition and boosted by administration of a boosting composition. The invention further relates to novel tetrameric soluble class I MHC/peptide complexes as a tool for directly monitoring vaccination regimens and determining novel epitopes.

Recent advances in our ability to monitor frequency of antigen CTL responses in ex-vivo assays are rapidly improving our capacity to compare different vaccination protocols. In particular, the use of tetrameric soluble class I MHC/peptide complexes (tetramers) provides an opportunity to greatly accelerate development of new vaccines by allowing rapid and accurate analysis of human CTL responses [1-3].

It has become clear that heterologous prime-boost vaccination protocols, based on repeated injections of non-cross reactive vectors encoding the same antigenic

protein, result in strong CTL responses, probably due to focusing of the immune response towards epitopes contained within the recombinant target proteins [4]. Recent results have demonstrated that combination of priming with plasmid DNA and boosting with recombinant defective vaccinia virus MVA generate high levels of specific immunity [5-10].

Alphaviruses have been extensively studied as viral vectors in vaccination protocols [11-15]. The replication incompetent alphavirus, Semliki Forest Virus (SFV), has proven to be capable of inducing antibodies and CTL directed against the encoded foreign antigens [14,15]. The small size of the SFV genome [16] makes this virus a very attractive vector for vaccination strategies, as expression of a small number of viral structural proteins maximise the chances of generating an immune response specific to recombinant proteins, rather than to viral structural proteins.

Several studies have demonstrated that viruses and tumour cells evade specific immune responses by mutating or deleting antigenic proteins [17,18]. In order to minimise the generation of virus or tumour antigen loss variants,

vaccine induced immune responses should be specific to a broad range of different epitopes, possibly encoded by distinct proteins. This rationale has led to the generation of vaccines encoding strings of CTL epitopes, aimed at simultaneously expanding CTL with different specificity. Vaccination of A2 transgenic mice has shown that multiple epitopes encoded within poly-epitope constructs can each prime specific CTL, suggesting the feasibility of this approach for immunotherapy clinical trials [19-22]. However, due to the technical limitations of assays for directly monitoring CTL responses in these mice, evidence is lacking that polyvalent constructs are capable of expanding CTL of many specificities to effective levels.

There is hope that poly-epitope vaccines will be capable of inducing broad based cytotoxic T lymphocyte (CTL) responses in humans. The administration of a plurality of epitopes is aimed at simultaneously expanding CTL with different specificity. Although such polyvalent constructs have proven capable of simultaneously priming CTL of multiple specificities in animals which is clearly advantageous, it remains unclear whether they are capable of subsequently boosting each of these CTL responses to effective levels.

It is known that some epitopes are more efficient at raising an immune response than others. Some epitopes may be described as dominant, i.e. they provoke a strong CTL response, while others may be described as subdominant in that they provoke a weaker response. However, when trying to raise an immune response to a broad range of epitopes it is important that the subdominant epitopes are not overlooked in favour of more dominant epitopes.

During the priming stage of a vaccine regimen the more dominant epitopes provoke a greater CTL response than the weaker epitopes. This means that after an initial priming event to a plurality of epitopes, the CTL response is inevitably greater for the more dominant species and weaker for the subdominant species. However, the present inventors have found that the situation is made worse when the same plurality of epitopes is administered as a poly-epitope construct during the boosting phase. This appears to be true even when the poly-epitope is provided in a different vector/vehicle than the priming phase. The inventors have found that during the boosting stage, the CTL response to the more dominant epitopes is increased at a greater rate than the CTL response to the subdominant epitope, to the extent that the expansion of

the CTL response to the subdominant epitopes is significantly reduced. This means that the CTLs raised to the dominant epitopes are expanded further at the expense of the CTLs raised to the subdominant epitopes. As a consequence, the proportion of CTLs raised to the dominant epitopes is increased whereas the proportion of CTLs raised to the subdominant epitopes is only marginally increased. This means that the boosting phase narrows the immune response by favouring proliferation of CTL expanded in the initial priming stage.

The present inventors have surprisingly determined a novel prime-boost regimen that helps to overcome the potentially negative effect of the boosting phase on a plurality of dominant and subdominant epitopes.

Remarkably, the inventors have found that a broad CTL response can be more uniformly boosted to effective levels if, following the priming stage, the epitopes are used individually to boost the response as opposed to being administered as a single poly-epitope construct. By boosting with the individual epitopes, the inventors have found that the CTLs raised against the dominant epitopes are not boosted at the expense of the CTLs raised against

the subdominant epitopes. Rather, they are boosted equally.

Specifically, and as exemplified below, the inventors have used DNA and viral vectors encoding a string of melanoma epitopes, to demonstrate that prime-boost vaccinations result in the expansion of a narrow CTL repertoire. At the boosting step the inventors found that CTL competition for recognition of cells presenting the poly-epitope construct skews the response towards those CTL expanded more efficiently during priming. In contrast, the inventors have found that simultaneous expansion of CTL specific to dominant and subdominant determinants is obtained when APCs were presenting the epitopes separately during the boosting phase. This could be accomplished, for example, by injecting a mixture of viruses each encoding a separate antigen or by injecting a mixture of APC presenting the epitopes separately.

Thus, the invention provides a method of inducing a specific but broad based CTL response to a plurality of epitopes, where poly-epitope constructs are used in the priming phase of a vaccination regimen but immunogens

encoding or comprising the epitopes individually are used for the boosting phase.

The invention also provides a heterologous prime-boost vaccination regimen where epitopes in the boosting phase are presented to the immune system in a different way than in the priming stage. This is explained in more detail below.

The present invention arises from the determination that the boosting phase is considerably more effective in inducing a specific but broad based CTL response to a plurality of epitopes if those epitopes are administered individually.

Thus, if an individual has already been primed by a plurality of epitopes, the invention provides a method of boosting the previously induced (primed) immune response comprising administering the plurality of epitopes individually, i.e. separately, on separate constructs or carried by separate vehicles.

In all aspects of the invention described herein, a plurality of epitopes may be taken to any number of epitopes greater than 2, more preferably, greater than 4

and still more preferably greater than 7. Of the plurality of epitopes, at least two, more preferably four and even more preferably seven epitopes will be different i.e. comprise a different amino acid sequence or be recognised by different antibodies. However, it is also preferably that the plurality of epitopes comprise many epitopes in the order of tens or hundreds. It is likely that some of these epitopes will be very similar and may cross-react.

Thus, if an individual has been infected by, or in some way come in contact with i.e. been exposed to, a pathogen (e.g. virus, bacteria etc) or a tumour, then the individual's immune system will have been naturally primed against a plurality of epitopes presented by the pathogen or tumour. However, this initial priming of the immune system may well be insufficient for the individual to mount an effective defence against the pathogen or tumour. However, in accordance with the present invention, the already primed immune response may be boosted by administering the plurality of epitopes individually, i.e. separately, carried by separate constructs (peptide or nucleic acid) or separate vehicles. Thus, in this context, the present invention has vast therapeutic potential.

Although it would be possible to detect whether an individual had been primed to a particular epitope, i.e. through exposure to a pathogen or as a result of a tumour, this step would not be necessary.

In order to save time, cost and trouble, it would be preferable to treat every patient suspected of having been primed to a plurality of epitopes by exposure to a pathogen or a tumour as a primed patient.

Accordingly, in a first aspect of the present invention, there is provided a method for boosting an immune response in an individual, said individual having been previously primed against or exposed to at least one of said plurality of epitopes, preferably all of said plurality of epitopes; said method comprising administering to the individual a plurality of constructs, each encoding or comprising one of said plurality of epitopes. The construct may be a nucleic acid sequence capable of encoding a peptide comprising the epitope in question or it may be a peptide or protein/polypeptide comprising the epitope which can be administered directly. The nucleic acid sequence may be DNA, RNA or cDNA capable of encoding a peptide comprising

one or more of the epitopes in question. Whether the construct is nucleic acid sequence encoding the peptide or a peptide itself, it is preferable to use a vehicle to carry the construct so that is can be efficiently presented to the individual's immune system. Preferably, the constructs are each presented or carried by separate vehicles such as a nucleic acid expression vector, e.g. a viral vector, or APC, e.g. dendritic cells or lymphocytes e.g. B cells. The vehicles may also act as adjuvants to help with the inducing immune response. The APCs may be used to express peptide constructs or they may be pulsed prior to administration.

The method in accordance with the first aspect of the present invention, may further comprise administering a "second" or further boosting composition. This composition will also comprise individual constructs, each comprising one of said plurality of epitopes. Again, the constructs may be peptides or nucleic acid sequences capable of encoding said peptides.

The administration of a second or further boosting composition has the benefit of not only further boosting the individuals immune response to the administered epitopes but also providing a "first" boost to any

epitopes present in the medicament that had not been already primed naturally by the individual through exposure to the pathogen or tumour. In other words, the second/further boosting composition ensures that any epitopes presented in the medicament ("first" boosting composition) that the individual had not previously been exposed to, would effectively be boosted for the first time.

Alternatively, the present invention may be used to immunise an individual against a pathogen or tumour associated antigen, i.e. as a preventative vaccine. In this situation, the individual's immune system must first be primed by a plurality of epitopes characteristic of the pathogen and then boosted to help the immune system raise an effective defence against the pathogen. This is known as a prime-boost regimen. However, as described above, the inventors have found that to maximise the immune response against each and every one of the epitopes, the epitopes must be administered individually in the boosting stage. Further, the inventors have also determined that a heterologous prime-boost regimen is preferable to the homologous prime-boost methods already described in the art. Thus, it also preferable to administer the plurality of epitopes during the boosting

stage using separate vehicles, e.g. viral vectors, that are different to and non cross-reactive with vehicles which may have been used in the priming stage.

Thus, in a second aspect of the present invention, there is provided a method of inducing an immune response, preferably a CD8+ T cell immune response, to a plurality of epitopes in an individual, said method comprising the steps of administering to the individual a priming composition comprising a construct encoding or comprising said plurality of epitopes and then administering a boosting composition which comprises a plurality of individual constructs each comprising one of said plurality of epitopes.

In accordance with the second aspect, the construct may be a peptide (protein/polypeptide) or a nucleic acid sequence encoding said peptide. it is also preferably, that the constructs are administered using a vehicle capable of efficiently displaying the epitopes to the individual's immune system. Thus, where the construct is a nucleic acid sequence, this may be contained within a nucleic acid expression vector, i.e. a plasmid or viral vector. These vectors may likewise be contained within a cell such as an Antigen Presenting Cell (APC).

Where the construct is a peptide, it may be preferable to use a cell, more preferably an APC as a vehicle as these cells are capable of displaying peptides efficiently to the immune system. Examples of APCs include dendritic cells and lymphocytes.

The administration of the constructs to an individual using vehicles is described in more detail below.

The priming composition may comprise one or more nucleic acid vectors, each containing nucleic acid encoding a plurality of epitopes. Alternatively, the priming composition may comprise peptides or antigens containing a plurality of epitopes.

In this second aspect, the priming composition comprises a string of epitopes, i.e. a polyepitope construct. However, the method may alternatively include the administration of one or more constructs encoding or comprising one or more of the plurality of epitopes. However, in this situation, it is preferable that the prime-boost regimen is a heterologous prime-boost regimen. In other words, if the priming composition comprises individual epitopes, the boosting composition

preferably carried or presents its individual epitopes using different and non-cross reactive vehicles.

For example, where nucleic acid constructs are used different viral vectors may be used in the priming and boosting phase. Likewise, for peptide constructs, different APC cells may be used between the priming and boosting phase, e.g. B cells for priming and dendritic cells for boosting.

This is a preferred embodiment of the invention and it must be appreciated that homologous prime-boost prime-boost regimens are also within the scope of the present invention, particularly when using peptide constructs.

It is also preferred that all priming nucleic acid constructs are recombinant constructs for example, any genetic constructs like recombinant viral constructs, DNA constructs, RNA constructs, or cells transfected or transduced with such constructs. Further the priming composition may comprise separate peptides or proteins and cells that are extra- or intracellularly loaded with such peptides or proteins. The peptides may form part of a fusion construct with a carrier protein or adjuvant. These may be produced as fusion proteins.

Where the boosting or priming compositions comprise peptides or proteins, these may be delivered using Antigen Presenting Cells (APCs) for example dendritic cells or lymphocytes (B cells), pulsed with peptide and/or protein (including intracellular delivery of peptides or proteins into the APC). The APCs once pulsed with peptide or protein may also be infected by virus in order to help activate the APC, i.e. the virus in this case acts as an adjuvant for the peptide.

Particles such as sepharose beads or chitine beads may also be used to mimic APCs and display peptide/MHC complexes and co-stimulatory molecules for stimulation of the immune system.

Exosomes or other subcellular bodies derived from APCs may also be pulsed with peptide and/or protein (including intracellular delivery of peptides or proteins into the exosomes) for delivery of the peptide epitopes.

It is also possible to administer the peptide or protein directly into the individual preferably at separate locations. The peptide or protein administered in this

way is preferably accompanied by an adjuvant in either the priming or boosting phases.

Where a nucleic acid vector is provided as a vehicle, it is preferable that the nucleic acid encoding the epitopes is operably linked to regulatory sequences for production of said antigen in the individual by expression of the nucleic acid.

As the priming composition presents a plurality of epitopes, a broad but specific CTL response is induced by the individual's immune system.

In contrast to the priming composition, the boosting composition presents the epitopes always individually. This overcomes the problem determined by the inventors that pre-existing memory CTL responses significantly reduce CTL response to other epitopes contained within the same construct during the boosting phase.

The priming composition if used, or the boosting composition when using nucleic acid constructs, may further comprise any vehicle for carrying the nucleic acid construct encoding the epitopes e.g. a viral vector, such as adenovirus vectors, Herpes simplex virus vectors,

vaccinia virus vector. The viral vector may be a modified, replication-deficient vector, e.g. modified virus Ankara (MVA), or it may be an avipox vector e.g. fowlpox, Canarypox and so on. Preferred vectors include the replication incompetent alphavirus Semliki Forest Virus (SFV). Other appropriate vectors will be apparent to those skilled in the art.

The priming composition may comprise DNA encoding the antigen. The DNA may be in the form of a circular plasmid that is not capable of replicating in mammalian cells. Expression of the antigen will preferably be driven by a promoter active in mammalian cells, e.g. cytomegalovirus immediate early (CMV IE) promoter.

The $CD8^+$ T cell immune response may be primed using a DNA vaccine, Ty-VLPs or recombinant modified Vaccinia virus Ankara (MVA). In the examples provided below, the inventors describe embodiments of the invention using a recombinant MVA naked plasmid DNA vaccinia virus; and semliki forest virus (SFV) during the priming phase. However, it will be apparent to the skilled person that other vectors, viral or otherwise, may equally be used.

As mentioned above, it is preferable to use a different, non-cross reactive vehicle, such as a nucleic acid expression vector, e.g. a viral vector, for displaying epitopes during the boosting phase than that used during the priming phase. In the examples provided below, plasmid DNA was used as a vehicle vector during the priming phase and vectors vaccinia, MVA and/or SFV were used as vehicles during the boosting phase. As multiple vectors will be used as vehicles during the boosting phase, these may be the same or different.

Thus, in accordance with the first and second aspect of the invention, there is provided a novel vaccination regimen that can be used as a method of vaccinating an individual against pathogens including self antigens or tumour antigens. Exemplified below are the use of NY-ESO-1, Tyrosinase and Melan-A antigens. However, other antigens will be known or may be determined by the skilled person.

Further, the invention has an important utility as a vaccination model for testing and establishing vaccination strategies or regimens. Thus, the vaccination model allows vaccination regimens to be

established which maximise a specific but broad based CTL response to a plurality of epitopes.

It is usual to test vaccine regimens on laboratory animals such as mice prior to testing on humans in clinical trials. Transgenic mice have been used in the past to test responses to particular antigens or epitopes. It is important to provide a biological environment that is as equivalent to the human environment as is possible. Therefore, transgenic mice are produced which have the ability to express human MHC molecules. In the examples provided below, the inventors have used two forms of transgenic mice.

Firstly, they have used HHD A2 transgenic mice which express a transgenic monochain histocompatibility class I molecule in which the C terminus of the human β2m is covalently linked to the N terminus of a chimeric heavy chain (HLA-A2.1 α1- α2, H-2D^b α3 transmembrane and intracytoplasmic domains). The H-2D^b and mouse β2m genes of these mice have been disrupted by homologous recombination resulting in complete lack of serologically detectable cell surface expression of mouse histocompatibility class I molecules.

Secondly, the inventors have used A2-K^b mice which express a chimeric heavy chain (HLA-A2.1 α1- α2, H-2K^b α3 transmembrane and cytoplasmic domains) in non-covalent association with mouse β2m.

Thus, both of these transgenic mice express a chimeric MHC where the α1 and α2 domains are derived from human A2 MHC and the α3 domain is from murine H-2K^b or H-2D^b. These mice are referred to as A2 transgenic mice. However, the present invention may equally well be performed on HLA-A1, HLA-A3 or HLA-A4 transgenic mice, i.e. any other murine model expressing human class I molecules in a similar way as A2 transgenic mice do.

Therefore, the invention further provides a method of testing a vaccination regime comprising the steps of administering a primary composition to a test animal, said primary composition comprising a nucleic acid encoding a plurality of epitopes under test, subsequently administering a boosting composition, said boosting composition comprising a plurality of nucleic acid vectors each containing one of the said plurality of epitopes under test; and determining the CTL response to each of the epitopes under test.

Preferably, the test animal will be a transgenic animal that provides an immune environment as close to the human immune environment as possible. The preferred test animal is an A2 transgenic mouse as described herein.

As discussed above, the priming vector preferably is a DNA plasmid or viral vector. However, the boosting vectors are preferably different to the priming vector. In a preferred embodiment the priming vector is DNA, and the boosting vector is selected from the group of vaccinia, MVA and/or SFV. SFV is the preferred vector for the boosting phase as the inventors have determined that excellent results are achieved when used following DNA priming vector or with MVA as the boosting vector. SFV does not cross-react with MVA and therefore these immunogen vectors can be effectively used together. The inventors have also found that the nucleic acid constructs whether as part of a viral vector or not, may be administered in association with a mammalian cell, such that the antigens are presented on its surface. Such cells are known as Antigen Presenting Cells (APCs) when antigen is presented on their surface. Thus, the term APC includes cells such as tumour cells. The use of APCs to carry the construct is particularly preferable during the boosting stage. Thus, possible boosting

reagents include APCs, such as dendritic cells or lymphocytes transfected or transduced with the viral or non-viral nucleic acid construct or tumour cells displaying antigen.

In particular embodiments of the first aspect of the present invention, administration of a priming composition is followed by boosting compositions, the priming composition and the boosting composition being different from one another, e.g. as exemplified below. However, a second and third boosting composition may be administered within the method of the present invention as mentioned above. In one embodiment, a triple immunisation regimen employs DNA expressing a plurality of epitopes; followed by SFV as a first boosting composition where a plurality of SFV vectors are used each comprising one of the plurality of priming epitopes; followed by MVA as a third boosting composition where a plurality of MVA vectors are used each comprising one of the plurality of priming epitopes. Alternatively, the SFV boosting composition may be administered after the MVA boosting composition.

Likewise, where peptides are administered directly, peptide pulsed APCs, exosomes or APC mimics may also be

used for several sequential boosting steps. This may be achieved by sequential injections.

In all cases, it is preferable to administer (e.g. by injection) the priming and boosting composition several times to ensure successful delivery.

Priming with vectors expressing a plurality of epitopes can be followed by a mixture of recombinant virus (i.e. either SFV or MVA) comprising one or more of the plurality of priming epitopes and followed by a further boosting based on the injection of peptides, each, encoding one of the plurality of priming epitopes. The peptides will preferably be between 5 and 15 amino acids in length, more preferably between 5 and 12 amino acids in length, more preferably between 5 and 10 amino acids in length. 9 amino acid long peptides are preferred. The peptides may be naturally occurring or they may be synthetic.

In order to enhance the method of testing vaccination regimens or strategy, the inventors have appreciated that accurate, efficient and fast testing of the provoked CTL response is required. With this is mind, the present inventors have developed a novel tetramer based technique

to directly monitor the frequency of HLA A2 restricted CTL expanded in vaccinated HLA A2 transgenic mice. In association with the first aspect of the present invention, this will greatly accelerate development of new vaccines by allowing rapid and accurate analysis of human CTL responses.

Specifically, the inventors have developed a technique for directly monitoring A2 restricted CTL responses in the blood of A2 transgenic mice by engineering chimeric A2 class I molecules containing the mouse $H2K^b$ alpha 3 domain. This technique allows accurate monitoring of the frequency of CTL induced by prime-boost regimens using poly-epitope constructs encoded within a number of different vectors and the correlation of the frequency of these CTL with their cytotoxic activity in vivo. This has the advantage of reducing the number of mice in each study considerably as they do not have to be killed for their CTL responses to be addressed.

Thus, in a further aspect of the invention, there is provided a multimeric MHC structure that is capable of detecting specific CTLs expanded following vaccination of an individual or test animal with one or more epitopes. The multimeric MHC structure comprises two or more MHC

molecules, preferably four molecules, held together in a single structure by a binding member such as streptavidin. The streptavidin used here may be fluorescently labelled for the detection of the CTLs binding the tetramer. As a plurality of MHC molecules are held in close proximity, they can by effectively used to display the epitope of interest in the form of a peptide so as to detect CTLs raised to that epitope. If effectively primed, the CTLs will recognise the displayed peptide/epitope and bind to the structure. This binding can be detected by known techniques such as flow cytometry, usually in combination with labelled antibodies e.g. anti CD8 antibodies.

However, the inventors have found that the use of these multimeric MHC structures, preferably tetramers, for testing the CTL responses in the vaccination model described above is limited as the MHC is of human origin whereas the test animal will be non-human, usually mouse, and therefore will have murine CD8 which does not effectively binding to human MHC.

To overcome this problem, the inventors have devised a chimeric multimeric MHC structure where the human $\alpha 3$ domain of the MHC is replaced with a murine $\alpha 3$ domain.

As the α3 domain binds the CD8 molecule, the chimeric multimeric MHC structure is more efficient at detecting the CTL response to the epitope under test than the non-chimeric structure.

Therefore, the invention further provides a chimeric multimeric MHC structure comprising at least two human MHC molecules held in close proximity by a binding member, wherein each MHC molecule contains an altered α3 domain so as to represent a murine α3 domain instead of a human α3 domain. Preferably, the human α3 domain is replaced by a murine α3 domain. The chimeric multimeric MHC structure may also be complexed with peptides displaying the epitope under test.

The murine α3 domain may be inserted into the human MHC to replace the human α3 domain, by creating a fusion protein, or by mutating the human α3 domain by insertion, deletion, or substitution of amino acids or nucleotides encoding amino acids characteristic of the murine α3 domain. Ideally, the chimeric MHC is produced as a fusion protein where nucleic acid encoding the human α1 domain and human α2 domains is expressed along with nucleic acid encoding the murine α3 domain. In this way a chimeric MHC fusion protein will be produced.

The multimeric chimeric MHC structure can then be associated with a peptide displaying the epitope under test. The number of peptides being displayed by the chimeric MHC will depend on the number of MHC molecules in the multimeric structure. The inventors have produced tetramers which will allow four peptides/epitopes to be displayed in close proximity. Thus, this structure can be used to detect the presence of a CTL response to the epitope in question. For example, the tetramer will display the peptide/epitope and when added to a biological sample (e.g. blood) obtained from the test animal, any CTLs recognising the epitope will bind to the tetramer with the aid of murine CD8. As the murine CD8 binds more successfully to murine α3 domain than human α3 domain, the binding of the CTL to the chimeric MHC tetramer according to the present invention is more stable than binding to a non-chimeric MHC tetramer.

The binding of the tetramer to the CTL can be detected by using, for example a fluorescently labelled tetramer. In addition, labelled CD8 antibody can be used to aid in the detection labelling and staining techniques are known to the skilled person.

As well as being extremely useful in monitoring the CTL response in accordance with the vaccination regimens mentioned above, the chimeric multimeric MHC structures can also be used to quickly and efficiently determine epitopes in a particular protein.

For example, A2 transgenic mice immunised with defined tumour or viral antigenic protein(s) encoded by DNA and/or recombinant viruses can be monitored for their ability to mount a specific CTL response by using the chimeric multimeric MHC class I molecules associated with peptides derived from the antigenic protein(s). This protocol will make possible the rapid identification of novel peptide epitopes encoded within antigenic proteins.

The inventors' findings are of importance for the design of optimised vaccines capable of simultaneously expanding high numbers of CTL specific for multiple epitopes. They are also important with regard to providing a vaccination model which allows quick, efficient and reliable testing of epitopes and allows design of the most efficient vaccination regimen.

The inventors have also devised a novel chimeric MHC multimer which can be used to efficiently detect a CTL response to a test epitope in a test animal.

Aspects and embodiments of the present invention will now be illustrated, by way of example, with reference to the accompanying figures. Further aspects and embodiments will be apparent to those skilled in the art. All documents mentioned in this text are incorporated herein by reference.

Brief Description of the Drawings

Table 1 Poly-CTL epitope construct. The poly-CTL epitope gene (mel3) was constructed as a single string of epitopes. Mel3 cassette was cloned into four distinct vectors: naked DNA, vaccinia virus WR, MVA and SFV.

Fig. 1 efficient processing and presentation of mel3 CTL. HLA A2 and HLA A1 positive B cells were infected with mel3. MVA and used as targets of CTL clones specific to each epitope contained within the mel.3 poly-CTL construct. Specificity of each CTL clone and percentage of specific lysis are shown above each panel. Target cells were pulsed with relevant peptide (+ peptide),

unpulsed (- peptide), infected either with mel3 MVA (MVA.mel3) or an irrelavant vaccinia (irr vac). Mouse NP 366-374 specific CTL were used as effectors cells against mouse MC57 fibroblasts infected with mel3.MVA.

Each bar corresponds to a different effector to target ratio: black bars 10:1, open bars 3:1 dotted bars 1:1.

Fig. 2 Ex-vivo frequency of NP 366-374 specific CTL in mice immunised with homologous and heterologous prime boost vaccination strategies. Each panel corresponds to a different vaccination procedure.

Fig. 3 Prime-boost of A2/Kb mice with DNA.mel3 followed by MVA.mel3.

A. Simultaneous generation of Db and A2 restricted CTL in A2/Kb transgenic mice. Mice were primed i.m. with DNA-mel3 and boosted 10 days later i.v. with MVA-mel3. Ex-vivo tetramer analysis of DB/NP366-374 and A2/melan-A 26-35 was carried out. Frequency of tetramer positive cells is shown in each vaccinated mouse after 3 days from MVA boost.

B. Effect of pre-existing memory CTL response specific to a single determinant contained within the poly-CTL epitope construct. A2/Kb mice were immunised

i.n. with influenza virus and subsequently injected with DNA.mel3 followed by MVA.mel3. Ex-vivo tetramer analysis of Db/NP366-374 and A2/melan-A 26-35 was carried out. Frequency of tetramer positive cells is shown in each vaccinated mouse after 3 days from MVA boost.

Fig. 4 Hierarchy of prime-boost vaccine driven CTL. HHD mice were primed with DNA.mel3 and boosted with either vac. Mel3 (A), MVA.mel3 (B) or SFV.mel.3 (C). Frequency of melan-A, tyrosinase and NY-ESO-1 specific responses were simultaneously measured by ex-vivo tetramer staining. DNA.mel3 primed SFV.mel3 boosted mice (group C) were injected with fluorochrome labelled splenocytes pulsed with either the melan-A, tyrosinase or NY-ESO-1 peptide. The percentage of in vivo killing is shown (D).

Fig. 5 Immunodominance of Melan-A specific CTL response can be overcome by poly-vaccinia boosting or by adoptive transfer of in vitro infected splenocytes. DNA.mel3 primed HHD mice were either boosted with a mixture of vaccinia viruses encoding the full length tyrosinase and full length NY-ESO-1 (A). Alternatively, DNA mel3 primed HHD mice were injected either with three aliquotes of splenocytes separately infected in vitro with full length tyrosinase, full length NY-ESO-1 and mel3. Vaccinia (B,

panels *a*, *b* and *c*) or with splenocytes infected with mel3 vaccinia (B, panels d, e and f). Frequency of melan-A, tyrosinase and NY-ESO-1 specific responses were simultaneously measured by ex-vivo tetramer staining.

Fig. 6 Poly-virus boosting overcomes the immunodominance of melan-A_{26-35} specific CTL. DNA.mel3 primed HHD mice were boosted with either a mixture of vaccinia viruses encoding the full length tyrosinase, full length NY-ESO-1 and SFV.mel3 (A) or with SFV.mel3 (B). Frequencies of melan-A_{26-35}, $tyrosinase_{369-377}$ and NY-$ESO\text{-}1_{157-165}$ specific responses were simultaneously measured by ex-vivo tetramer staining. Staining of a single mouse out of six is shown. C and D: Each mouse was injected with fluorochrome labeled splenocytes pulsed with either the melan-A_{26-35}, $tyrosinase_{369-377}$ or NY-$ESO\text{-}1_{157-165}$ peptide and the % of in vivo lysis was calculated. Panel C corresponds to the in vivo killing in DNA.mel3 primed HHD mice boosted with a mixture of vaccinia viruses encoding the full length tyrosinase, full length NY-ESO-1 and SFV.mel3, while panel D corresponds to the in vivo killing in DNA.mel3 primed HHD mice boosted with SFV.mel3.

Fig. 7 The experiment shows $A2K^b$ tetramer stains from mice primed with MVA.mel3 and boosted with peptide pulsed dendritic cells (DCs). Two groups of mice are shown: Group A (three mice) received DCs pulsed with a mixture of 3 peptides (Melan-A, Tyrosinase and NY-ESO-1), and Group B (four mice) received a mixture of DCs pulsed with single peptides. On the left hand side of the figure, one individual response to three epitopes is shown from one mouse in each group. On the right hand side of the figure the average percentage of tetramer positive CTL in each group is shown. The error bars indicate the standard deviation of the mean. The experiment shows that peptide pulsed DCs can efficiently boost poly valent CTL responses primed by recombinant MVA (compare Fig. 4A, B and C) The experiment further demonstrates, that a mixture of separately peptide pulsed DCs for boosting is more efficient in boosting a poly-valent response when compared to DCs pulsed with a mixture of peptides.

Detailed Description

Materials and methods

Plasmid DNA construct

The DNA vector pSG2, used throughout the study, was

derived from pRc/CMV (Invitrogen, Paisley, UK) by removing the BamH1 fragment that contains the SV40 origin of replication and neomycin resistance marker and replacing the CMV promoter with a longer version of the same promoter containing intron A. The resulting plasmid contains the CMV promoter with intron A for expression in eukaryotic cells, followed by a multiple cloning site and the bovine growth hormone poly-A sequence. The plasmid is incapable of replication in mammalian cells. The gene encoding the mel3 sequence (**Table 1**) was introduced into the multiple cloning site using standard methods. Plasmid DNA for injection was purified using anion-exchange chromatography (Qiagen, Hilden, Germany) and diluted in phosphate buffered saline (PBS) at 1 mg DNA/ml.

Generation of recombinant Vaccinia virus and MVA

Recombinant and non-recombinant MVA were routinely propagated and titrated in chicken embryo fibroblasts (CEF) grown in minimal essential medium supplemented with 10% foetal calf serum (FCS). Recombinant MVA were made as described by cloning the mel3 poly-epitope string (**Table 1**) into the vaccinia shuttle vector pSC11. CEF infected with MVA at a multiplicity of 0.05 pfu per cell were transfected with lipofectin (Gibco) and shuttle plasmid as described [23]. The Vaccinia P7.5 promoter drives

expression of the polyepitope. Recombinant MVA were plaque purified 8 times.

Vaccinia viruses (WR strain) expressing mel3, full length NY-ESO-1 (kindly provided by Dennis L. Panicali, Therion Biologics Corporation, MA 02142, USA) or tyrosinase were made by cloning the mel3 poly-epitope construct, the NY-ESO-1 and tyrosinase full length cDNA into the thymidine kinase gene using the vector pSC11 as previously described [24].

Generation of recombinant SFV

The mel3 poly-epitope string was cloned into the transfer vector pSFV4.2-mel3. RNA produced from this vector was used to construct recombinant SFVmel3 particles. Recombinant SFV stocks were made and purified as described previously [16].

Generation of human CTL Clones and CTL assays

Human CTL clones were isolated as described [25]. Briefly, tetramer/CD8 double positive stained CTL cultures were sorted as single cells into U-bottom 96-well plates, previously coated with anti-CD3 and anti CD28 both at 100ng/ml in PBS, containing 10^5 irradiated B cells in Iscove's medium supplemented with 5% human serum, 100

U/ml IL-2. Proliferating clones were expanded to > 10^7 cells and used as effectors for standard Cr^{51} release assays. The inventors used JY B cells infected with MVA mel3 as targets for HLA A2 restricted CTL; XY B cells for HLA-A1 restricted epitopes and H-2b positive MC57 cells as targets for the D^b restricted Influenza Nucleoprotein. We titrated CTL clones in three fold dilutions against targets

Tetramer synthesis

Fluorescent tetrameric HLA-A2.1/peptide complexes were synthesised as previously described [1]. A2-Kb/peptide complexes were synthesised in an analogous fashion using a chimeric heavy chain of α1 and α2 domain of the A2.1 molecule and the α3 domain of the H-$2D^b$ molecule with human β2-micro globulin.

Isolation of PBL and Tetramer stains

Fresh PBL were isolated from blood taken from tail vein using red cell lysis buffer (Invitrogen, Paisley, UK). For tetramer stains $3x10^5$ cells were resuspended in 20 µl RPMI 1640 (Sigma, St Louis, MO) supplemented with 10% FCS. Cells were incubated with tetramer for 15 minutes at 37°C. PBL were then incubated with rat anti mouse CD8α

(Pharmingen, San Diego, CA) for 15 minutes at 4°C. Cells were washed twice in PBS and resuspended in PBS for FACScan (Becton Dickenson, Mountain View, CA) analysis.

Animals and Immunization protocols

HHD mice express a transgenic monochain histocompatibility class I molecule in which the C terminus of the human β2m is covalently linked to the N terminus of a chimeric heavy chain (HLA-A2.1 α1- α2, H-2D^b α3 transmembrane and intracytoplasmic domains) [20]. The H-2D^b and mouse β2m genes of these mice have been disrupted by homologous recombination resulting in complete lack of serologically detectable cell surface expression of mouse histocompatibility class I molecules. A2-K^b mice express chimeric heavy chain (HLA-A2.1 alpha 1 alpha 2, H-2 K^b alpha 3 transmembrane and cytoplasmic domains) in non-covalent association with mouse β2m. They additionally express a full set of C57BL/6-derived (H-2^b) class 1a and 1b mouse histocompatibility molecules [26]. All A2 transgenic mice used were bred in the inventors' animal facility. Female C57/BL6 mice 4-6 weeks old were obtained from Harlan Orlac (Shaws Farm, Blackthorn, UK). Plasmid DNA (25-50 μg/muscle) was dissolved in PBS and injected into each musculus tibialis under general

anaesthesia. 10 days after DNA injection, mice were boosted with recombinant vaccinia viruses, which were diluted in PBS and 10^6-10^7 pfu and injected intravenously (i.v.) into the lateral tail vein. Alternatively freshly isolated spleen cells were separately infected (multiplicity of infection of 5) with mel3, full length tyrosinase and NY-ESO-1 vaccinia for 90 minutes in RPMI supplemented with 0.1% BSA at 37°C. Cells were washed 3 times and re suspended in sterile PBS at a concentration of 6x 10^7 cells/ml combined and injected into lateral tail vein. Mice received 6x10^6 spleen cells.

Mice primed with influenza virus A (PR8) were infected by intra-nasal influenza injection (20 HAU/mouse). 30 days later mice were injected with DNA.mel3 followed by MVA.mel3, as described above. For priming or boosting with SFV-mel3 10^8 virus particles were diluted in sterile PBS and injected into the lateral tail vein.

In vivo killing

Freshly isolated spleen cells from HHD mice were separately incubated in RPMI medium with different peptides at a concentration of 10^{-6}M for 2 h. Each cell pool was then labelled with a different concentration of carboxyfluorescein diacetate succinimidyl ester (CFSE,

Molecular Probes, Eugene, Oregon) to allow simultaneous tracking of the different populations in vivo [27], Hermans, I.F., Yang, J. and Ronchese, F. Unpublished results. Labelled cells were pooled and injected at 10^7 cells/mouse into the tail vein. A control population without peptide that had been labelled with 5-(and-6-)-(((4-chloromethyl)benzoyl)amino)tetramethylrhodamine (CellTracker Orange, Molecular Probes, Eugene, Oregon) was co-injected to assess killing of peptide pulsed targets relative to unpulsed cells. Mice were bled at the time of injection of flurochrome labelled targets to determine their CTL frequencies to different epitopes. Disappearance of peptide/flurochrome labelled cells was tracked using FACS analysis of freshly isolated PBMC 5 h after the injection. Percentage killing was calculated relatively to the unpulsed population labelled with Cell Tracker Orange. 100- (100x(%pulsed/%unpulsed)). WinMDI 2.8 and CellQuest 3.3 software was used to analyse the facs data.

Results

A string of 5 HLA-A2 and 2 HLA-A1 melanoma epitopes was cloned into four distinct vectors: a) naked plasmid DNA (mel3. DNA); b) vaccinia virus (mel3-vaccinia); c)

Modified Vaccinia Ankara virus (mel3. MVA); d) Semliki Forest Virus (mel3-SFV). To ensure monitoring of CTL responses restricted by human and mouse class I molecules, the inventors introduced an additional epitope from the influenza Nucleoprotein (NP) restricted by H-2Db class I molecules. Since they had previously shown that presentation of amino-terminal NP366-374 epitope can be affected by neighbouring amino acid residues 24, the inventors decided to express the influenza NP 366-374 epitope at the carboxyl terminal end of the poly-epitope construct. Sequence of the poly-epitope constructs used in the paper are shown in **Table 1.**

Efficient presentation of MVA encoded poly-epitopes

Initial experiments were carried out to compare the A2 binding affinity of each epitope contained within the mel.3 construct. The results of these experiments demonstrated that mel3 peptide epitopes had a broad range of binding affinities for A2 molecules. The Melan-A 26-35 peptide analogue ^{28} had the highest binding affinity, while the NY-ESO-1 157-165 and tyrosinase 1-9 peptides had a significantly lower affinity, as defined by their ability to inhibit at different concentrations presentation of the influenza Matrix epitope 58-66 (data not shown). The inventors and others have previously

demonstrated that optimal flanking residues are important to ensure presentation of class I restricted epitopes 24,29. To establish that mel.3 peptide epitopes were properly processed, and to assess that competition for binding to A2 molecules did not impair CTL recognition of lower affinity epitopes, they infected target cells with mel.3 vaccinia and demonstrated that each of the 7 epitopes contained within the poly-epitope mel.3 cassette was simultaneously presented to specific CTL (**Fig. 1**). The inventors had previously shown that proteasome dependent degradation impairs presentation of the MAGE3 A2 epitope 271-279 [30]. It was therefore surprising to observe that infection of target cells with mel3 vaccinia was capable of sensitising them for lysis by MAGE3 271-279 specific CTL. Further experiments demonstrated that processing of the MAGE3 271-279 epitope contained within the mel3 construct, unlike its processing within the full length MAGE3 protein, was lactacystein resistant and TAP independent (data not shown), consistent with processing of mel.3 construct by Endoplasmic reticulum resident proteases.

Influenza NP 366-374 specific CTL responses in mice vaccinated with poly-epitope encoded vaccines

Efficient presentation of the NP366-374 epitope by mel3 vaccinia infected cells prompted the inventors to assess in C57/B6 mice the ability of different vaccination strategies to induce a strong NP366-374 specific CTL response (**Fig. 2**). Ex-vivo monitoring of the NP specific CTL response was carried out in PBL using Db/Influenza NP366-374 tetramers. The inventors compared homologous vs heterologous prime boost vaccination protocols (**Fig. 2**), and analysed the kinetics of CTL induction by DNA or MVA priming (data not shown). The results of these experiments confirmed that heterologous vaccination strategies are capable of inducing long lasting vaccine driven CTL responses, with frequencies up to 100 times greater than frequencies obtained by strategies based on repeated injections of the same antigen delivery system (**Fig. 2**).

Expansion of A2 restricted CTL in A2 transgenic mice

To test the ability of the mel.3 poly-epitope constructs to prime A2 restricted CTL responses in vivo, A2 transgenic mice were primed by DNA-mel.3 and boosted by MVA-mel.3, vaccinia mel.3, or SFV-mel3.

Initial experiments were carried out using A2.1 transgenic mice, which express chimeric A2.1 molecules containing the Kb α3 domain, and endogenous D^b and K^b molecules (A2/Kb mice) [26]. To enable monitoring of the A2 restricted responses at the same time as the D^b restricted Influenza NP366-374 response, the inventors employed novel A2/Kb tetramers, which were also capable of detecting the relevant CTL directly in PBL. Simultaneous staining with A2/Kb and D^b tetramers demonstrated that priming of A2/Kb mice with DNA.mel3, followed by MVA-mel.3, induced melan-A 26-35 and Influenza NP 366-374 specific CTL responses (**Fig. 3**). In contrast, responses specific to other mel.3 epitopes were not detectable by ex vivo tetramer stainings (data not shown).

The ability to simultaneously monitor CTL responses against the influenza NP epitope 366-374 and melan-A epitope 26-35 prompted the inventors to study whether previous exposure to influenza virus may compromise the ability of prime-boost protocols to expand melan-A 26-35 specific CTL in A2-Kb mice. In order to generate a strong NP366-374 specific CTL response, A2 transgenic mice were immunised with influenza virus and subsequently received DNA.mel3 followed by MVA-mel3 (**Fig. 3**). The results of these experiments demonstrated that expansion of NP366-

374 specific CTL, prior vaccination with mel3 poly-epitope constructs, significantly reduced the expansion of melan-A specific CTL (**Fig. 3**). The inhibitory effect of pre-existing flu specific CTL on the ability of mel3 prime-boost to induce melan-A specific CTL response (**Fig. 3**) raised the possibility that T cell interference during heterologous vaccination strategies may compromise the induction of a broad range immune response. The presence of endogenous mouse class I molecules significantly narrows the A2 restricted repertoire in A2Kb mice, hence hampering the ability to study the interplay between A2 restricted CTL specific to different vaccine encoded determinants.

This reasoning led the inventors to monitor the hierarchy of vaccine driven CTL responses upon prime boost protocols in the A2 transgenic mice HHD [20]. HHD mice, unlike A2Kb transgenic mice, express A2.1 class I molecules linked to human ß-2 microglobulin in a Db-/- and ß-2m-/- background, and have a much larger A2 restricted T cell repertoire than A2/Kb transgenic mice [20].

<u>Prime-boost vaccination of HHD mice induces large numbers of melanoma specific CTL</u>

Priming of HHD mice with DNA.mel3 led to the expansion of Melan-A specific CTL to frequencies detectable by ex-vivo tetramer staining in all vaccinated mice (data not shown). In contrast, expansion of NY-ESO-1 and tyrosinase specific CTL was only detectable in a small proportion of immunised mice, while responses to the Tyrosinase 1-9 and Mage3 271-279 were not detected in blood tetramer stainings (data not shown).

Additional experiments confirmed that NY-ESO-1 specific CTL responses were primed by DNA.mel3 injection, as shown by the significant NY-ESO-1 CTL response in DNA.mel3 primed mice boosted with vaccinia virus encoding the full length NY-ESO-1 (data not shown). In contrast, injection of NY-ESO-1 vaccinia virus, without priming with DNA.mel3, led to a much lower frequency of NY-ESO-1 CTL. Similar results were obtained upon injection of tyrosinase vaccinia in mice primed with DNA mel3 (data not shown).

The observation that the melan-A 26-35 specific CTL was the dominant vaccine driven CTL response after a single DNA vaccination, presented an opportunity to study the interplay between CTL specific to different vaccine encoded determinants in prime-boost vaccination

protocols. The inventors observed that boosting of DNA.mel3 primed HHD mice with either vaccinia.mel3 (**Fig. 4a**), MVA.mel3 (**Fig. 4b**), or SFV-mel3 (**Fig. 4c**), led to the expansion of melan-A specific CTL, up to 70-80% of total CD8+ T cells. Although responses specific to NY-ESO-1 and tyrosinase epitopes were significantly lower than the Melan-A specific responses, their frequencies ranged between 2 and 30% of CD8+ T cells, confirming that DNA priming and boosting with either replication competent (i.e. Vac.mel3) or incompetent viruses (MVA.mel.3 and SFV-mel3) significantly enhance the frequency of CTL specific to three distinct melanoma specific epitopes. The inventors confirmed that vaccine driven CTL were cytolytic, as shown by their ability to kill fluorochrome labelled splenocytes pulsed with relevant peptides in vivo (**Fig.4d**). These results demonstrated that the cumulative response specific to melan-A, NY-ESO-1 and tyrosinase in HHD mice primed with DNA.mel3 and boosted with three distinct viral vectors accounted for the specificity of the majority of CD8+ population.

Competition of vaccine driven CTL for mel.3 expressing APC

Since the inventors demonstrated the inhibitory effect of

a pre-existing flu memory CTL response on the ability to induce melan-A specific CTL (**Fig. 3**), they sought to study whether the high numbers of melan-A specific CTL, dominating the immune response after DNA priming, were capable of interfering with the expansion of NY-ESO-1 and tyrosinase specific CTL during the virus boosting.

It is known that competition for antigen recognition on the surface of antigen presenting cells leads to the immunodominance of higher frequency CTL populations [31-33]. The inventors reasoned that the higher numbers of melan-A CTL after DNA.mel 3 priming may lead either to rapid killing or shielding of mel3 vaccinia infected APC in vivo, resulting in a hampered stimulation of CTL specific to NY-ESO-1 and tyrosinase epitopes expressed by the same APC population.

This reasoning led them to assess whether a higher frequency NY-ESO-1 and tyrosinase specific CTL responses could be obtained by separating the APC expressing NY-ESO-1 and tyrosinase proteins from the APC expressing the mel3 construct. The results of these experiments confirmed this hypothesis, as shown by: **1)** expansion of NY-ESO-1 and Tyrosinase specific CTL in DNA.mel3 primed mice and boosted with a mixture of vaccinia viruses,

encoding the full length tyrosinase and full length NY-ESO-1 proteins (**Fig. 5a**); **2)** simultaneous expansion of melan-A, NY-ESO-1 and tyrosinase specific CTL upon adoptive transfer into DNA.mel3 primed mice of three aliquotes of splenocytes infected ex-vivo with vaccinia viruses encoding full length NY-ESO-1, tyrosinase and mel3 construct (**Fig. 5*b*, *panels a,b and c***), while adoptive transfer of splenocytes infected with mel3 vaccinia led to the expansion of Melan-A specific CTL (**Fig 5*b* panels *d*, *e* and *f***).

The inventors have demonstrated that boosting of DNA.mel3 primed mice with a mixture of recombinant viruses, encoding the full length tyrosinase, full length NY-ESO-1 and the mel3 construct, led to the simultaneous expansion of melan-A_{26-35}, NY-ESO-$1_{157-165}$ tyrosinase$_{369-377}$ specific CTL (**Fig. 6*a* *and* *b***). The identification of successful vaccination strategies to simultaneously expand large numbers of CTL with a broad specificity has important clinical applications, as we showed that T cell immunity induced by this type of optimised boosting strategies provides a more efficient in vivo killing of target cells than vaccinations based on poly-epitope prime boost strategies (**Fig. 6 *c* and *d***).

Immunodominance of Melan-A specific CTL could be broken by separating the antigens during the boost. When separately infected splenocytes were used to boost a polyvalent response relevant peptides were separately presented and resulted in simultaneous expansion of Melan-A, Tyrasinase and NY-ESO specific CTL. To simplify this approach the inventors used peptide pulsed dentritic cells to boost an MVA.mel3 primed response. The cells used for boosting were either pulsed with a mixture of peptides (**Fig. 7a**) or separately pulsed (**Fig. 7b**). The inventors show that separate pulsing of APC is superior to pulsing APC with a mixture of peptides. This approach also demonstrates, that poly-epitope constructs encoded in vaccinia virus can efficiently prime and APC pulsed with peptide can efficiently boost a polyvalent CTL response.

Discussion

There is a tremendous momentum in vaccine development, as recent advances in the monitoring of antigen specific CTL responses in ex-vivo assays are rapidly improving our capacity to compare different vaccination protocols. In order to minimise the generation of tumour and virus antigen escape variants, it is important to ensure the expansion of vaccine driven CTL specific to several

epitopes, including both dominant and subdominant determinants. Several papers have dissected the causes responsible for immunodominance of CTL specific to viral [34-36], and histocompatibility antigens [33,37,38]. However, it remains to be established how optimal vaccine strategies can lead to the simultaneous expansion of CTL specific to dominant and subdominant epitopes.

To address these questions the inventors engineered 4 distinct vectors encoding a string of melanoma CTL epitopes (**Table 1**), and compared in A2 transgenic and wild type B6 mice the ability of different vaccination strategies to elicit vaccine specific CTL responses. In order to identify strategies capable of expanding CTL specific to dominant and subdominant determinants, peptide epitopes with high and low binding affinity for A2 molecules were linked in the same construct. More specifically, the inventors included the modified melan-A analogue 26-35, previously shown to have an enhanced immunogenicity in vivo [28] and the NY-ESO-1 peptide 157-165, shown to have a much lower binding affinity to A2 molecules [39] (**Table 1**).

Vaccine driven CTL Hierarchy in mel3 vaccinated mice

The inventors have developed a novel tetramer based

technique to directly monitor the frequency of A2 restricted CTL expanded in A2 transgenic mice vaccinated in a prime-boost regimen. To increase the binding affinity of mouse CD8 to A2 molecules, they engineered A2 molecules containing the mouse H-2K^b alpha 3 domain (A2/K^b molecules), and demonstrated that tetrameric A2K^b molecules have an increased staining efficiency for mouse A2 restricted CTL and can identify A2 restricted responses in a large proportion of A2 transgenic mice, as compared with tetrameric A2 molecules.

While studying the immune response in A2Kb mice, the inventors have demonstrated that expression of Db molecules results in a strong influenza NP366-374 specific response, which significantly impairs the expansion of CTL specific to other mel3 encoded epitopes. In order to study the interplay between A2 restricted CTL specific to different vaccine encoded determinants, the inventors immunised the A2 transgenic mice HHD 20, which, unlike A2Kb transgenic mice, express A2 molecules in a Db-/- background.

Although several papers have recently studied the immune response in A2 transgenic mice vaccinated with poly-epitope constructs 19,20,40, this is the first publication in which the hierarchy of poly-epitope vaccine driven CTL in A2 transgenic mice has been

monitored by ex-vivo tetramer staining.

The inventors compared several vaccination strategies and confirmed that immunisations based on the injection of non-cross reactive vectors (heterologous prime-boost protocols) ensure higher levels of vaccine specific immune responses than immunisations based on the injections of homologous vectors (**Fig. 2**). The presence of neutralising antibodies against viral structural proteins and the presence of CTL specific to viral proteins may account for the lower CTL responses in mice vaccinated with repeated injections of the same virus, as compared with CTL frequencies upon vaccination with non-cross reactive vectors (**Fig. 2**). It has been suggested that the limited number of proteins encoded by plasmid DNA ensures that DNA priming focuses the immune response towards the recombinant protein, while virus boosting successfully expand this response, resulting in high levels of CTL specific to the recombinant protein. However, the inventors have shown that priming with either MVA.mel3 or SFV.mel3 led to a significant expansion of NP366-374 specific CTL upon boosting with influenza virus or MVA.mel3, respectively (**Fig. 2**), demonstrating that the ability to prime CTL is not unique to DNA vectors.

In HHD A2 transgenic mice, due to the lack of CTL

restricted by endogenous mouse class I molecules, heterologous prime boost resulted in a tremendous expansion of melan-A specific CTL up to 90% of total CD8+ T cells **(Fig. 4a)**, hence redirecting a large proportion of HHD mice's A2 restricted repertoire towards vaccine encoded CTL determinants. Several factors may contribute to the immunodominance of the melan-A specific CTL response. It is possible that a combination of an increased binding affinity for A2 molecules and for TCR, together with a favourable intracellular processing, may skew CTL responses towards the melan-A epitope 26-35 in DNA.mel3 primed mice.

Previous studies have shown that " suppression" of T cell responses specific to non dominant epitopes by T cell responses specific to dominant epitopes is observed only when both types of determinants are presented on the same APC [32,33,38]. Injection of large numbers of APC resulted in the expansion of T cells specific to the sub-dominant epitopes 41. The inventors have demonstrated that immunodominance of the melan-A epitope 26-35 was overcome by boosting strategies based on the injection of either a mixture of different recombinant viruses (**Fig. 5a**) or splenocytes infected in vitro by individual vaccinia viruses encoding full length proteins, rather than a poly-epitope construct (**Fig. 5b**).

Implications for vaccination strategies in patients.

These results are of importance, since several clinical trials are currently using heterologous prime boost vaccination protocols with poly-epitope constructs. While the inventors confirm the ability of heterologous prime-boost protocols in eliciting large numbers of vaccine specific CTL, they demonstrate that during heterologous prime-boost protocols, frequency of immunodominant CTL responses is significantly expanded over frequency of CTL responses specific to less dominant determinants. Although there are numerous mechanisms which may account for a narrowing of the CTL repertoire which responds to a vaccine, the inventors' results are consistent with a model of immunodominance based on competition of T cells for antigen presenting cells (APCs) 32,33,38. It is worth noting that the injection of vac.mel3 into naïve mice induces lymphocytocis with a shift of CD8+ frequency from 0.5% up to 30%, indicating a strong CTL response to the vaccinia virus. Of the CD8+ T cells induced in the blood as many as 50% are specific for Melan-A 26-35 (data not shown), demonstrating that melan-A 26-35 is one of the most immunodominant epitopes expressed by the virus amongst more than 200 vaccinia proteins responsible for the viruses' structure,

transcription and replication. This observation has important clinical implications for the design of viral-based vaccines encoding the Melan-A epitope 26-35. The use of recombinant SFV in prime-boost protocols is very attractive, as the inventors have demonstrated that SFV can be used both as priming vector in combination with MVA (**Fig. 2**) and for boosting in combination with DNA (**Fig. 4*C***). These results compliment a recently published report demonstrating in macaques the enhancement of simian immunodeficiency virus-specific immune responses induced by priming with recombinant SFV and boosting with MVA 11.

The inventors demonstrated that pre-existing memory CTL responses significantly reduce CTL responses specific to other epitopes contained within the same construct (**Fig. 3*b***). As several groups have used immunodominant influenza peptide epitopes as positive controls during vaccination trials, the inventors' result suggest that DNA or virus based vaccines should not encode epitopes expressed by recurrent viruses, as pre-existing memory CTL response may compromise the induction of CTL responses specific to other vaccine encoded CTL determinants.

The inventors have further shown that T cell competition is likely to play a role in modifying T cell responses in prime-boost vaccination strategies. The inventors' work strongly suggests that simulataneous presentation of different epitopes to a skewed repertoire of primed CTL leads to dominant expansion of a single CTL specificity. However, boosting the primed response with APC separately presenting the epitopes results in comparable expansion of CTL of multiple specificities to effective levels in vivo.

Thus, the present inventors have, amongst other things provided a novel system for dissecting the ability of different vaccination protocols to optimally induce polyvalent A2-restricted CTL responses. In accordance with the present invention, methods for inducing a broad-based CTL response should restrict the use of polyvalent constructs to the priming phase and use separate vectors encoding individual epitopes, or separate proteins/peptides for the boosting phase.

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Table 1

Nucleotide and amino acid sequence of mel.3 construct	Antigen	Epitope	Restriction
aga-tct-gcc-gcc-acc--			
atg-tta-cta-gct-gtt-ttg-tac-tgc-ctg- M L L A V L Y C L	Tyrosinase	1-9	(A2)
gaa-cta-gca-ggg-atc-ggc-ata-ttg-aca-gtg- E L A G I G I L T V	Melan-A	26-35(*)	(A2)
tat-atg-gat-gga-aca-atg-tcc-cag-gta- Y M D G T M S Q V	Tyrosinase	369-377	(A2)
gga-tct- G S	(Linker)		
gaa-gtc-gat-cca-atc-gga-cat-ttg-tac- E V D P I G H L Y	Mage-3	167-175	(A1)
ttc-ctg-tgg-ggt-cca-aga-gcc-ctc-gtt- F L W G P R A L V	Mage-3	271-279	(A2)
gaa-gca-gac-ccc-acc-gga-cac-tcc-tat- E A D P T G H S Y	Mage-1	161-169	(A1)
gga-tct- G S	(Linker)		
cag-ctt-tcc-ctg-ttg-atg-tgg-atc-acg-cag-tgc-ttt-ctg- Q L S L L M W I T Q C F L	NY-ESO-1	155-167	(A2)
gct-tca-aat-gaa-aac-atg-gat-gct-atg-tga A S N E N M D A M	Influenza Nucleoprotein	366-374	(Db)

(*) this sequence corresponds to the peptide analogue modified at position 2 (Men et. al.)

Claims:

1. Use of a plurality of epitopes in the preparation of a medicament for boosting an immune response in an individual, said individual having been previously exposed to at least one of said plurality of epitopes; said medicament comprising a plurality of peptides, each peptide comprising one of said plurality of epitopes.

2. Use according to claim 1 wherein said individual has been previously exposed to at least one of said plurality of epitopes either naturally or by administration of one or more of said epitopes.

3. Use according to claim 1 or claim 2 wherein said immune response is a CD8+ T cell immune response.

4. Use according to any one of the preceding claims wherein each peptide is associated with an antigen presenting cell.

5. Use according to claim 4 wherein the antigen presenting cell is a dendritic cell.

6. Use according to claim 4 wherein the antigen present cell is a lymphocyte.

7. Use according to any one of the preceding claims wherein the medicament further comprises an adjuvant.

8. Use according to claim 1 or claim 2 wherein each peptide is displayed on the surface of a cell.

9. Use of a plurality of epitopes in the preparation of first and second medicaments for inducing an immune response in an individual, said first medicament being a priming composition comprising a one or more peptides each peptide comprising one or more of said plurality of epitopes; and said second medicament being a boosting composition which comprises a plurality of peptides each peptide comprising one of said plurality of epitopes, wherein the second medicament is administered after the first medicament.

10. Use according to claim 9 wherein the immune response is a CD8+ T cell immune response.

11. Use according to claim 9 or claim 10 wherein each peptide is associated with an antigen presenting cell.

12. Use according to claim 11 wherein the antigen presenting cell is a dendritic cell.

13. Use according to claim 11 wherein the antigen presenting cell is a lymphocyte.

14. Use according to any one of claims 9 to 13 wherein the first and/or second medicament comprise an adjuvant.

15. Use according to any one of the preceding claims wherein said plurality of epitopes are derived from one or more pathogens

16. Use according to any one of claims 1 to 14 wherein said plurality of epitopes are derived from a tumour cell.

17. A method of boosting an immune response to a plurality of epitopes in an individual, said individual having been previously exposed to at least one of said plurality of

epitopes; said method comprising the steps of administering to the individual a composition comprising a plurality of peptides each peptide comprising one of said plurality of epitopes.

18. A method according to claim 17 wherein the individual has been previously exposed to at least one of said plurality of epitopes either naturally or by administering one or more peptides comprising one or more of said epitopes.

19. A method according to claim 17 or claim 18 wherein the individual is a test animal and the epitopes are test epitopes.

20. A method according to claim 15 further comprising the step of determining the CTL response to each of the epitopes under test.

21. A method according to claim 19 or claim 20 wherein the test animal is a transgenic animal that provides an immune environment close to the human immune environment.

22. A method according to claim 21 wherein the test animal is an A2 transgenic mouse.

23. A method according to any one of claims 17 to 22 wherein each peptide is associated with an antigen presenting cell.

24. A method according to claim 23 wherein the antigen presenting cell is a dendritic cell.

25. A method according to claim 23 wherein the antigen presenting cell is a lymphocyte.

26. A method of inducing an immune response to a plurality of epitopes in an individual, said method comprising the steps of administering to the individual a priming composition comprising one or more peptides comprising one or more of said plurality of epitopes and then administering a boosting composition which comprises a plurality peptides each encoding one of said plurality of epitopes.

27. A method according to claim 26 wherein the individual is a test animal and the epitopes are test epitopes.

28. A method according to claim 27 further comprising the step of determining the CTL response to each of the epitopes under test.

29. A method according to claim 27 or claim 28 wherein the test animal is a transgenic animal that provides an immune environment close to the human immune environment.

30. A method according to claim 29 wherein the test animal is an A2 transgenic mouse.

31. A method according to any one of claims 26 to 30 wherein each peptide is associated with an antigen presenting cell.

32. A method according to claim 31 wherein the antigen presenting cell is a dendritic cell.

33. A method according to claim 31 wherein the antigen presenting cell is a lymphocyte.

34. A chimeric multimeric MHC structure that is capable of detecting specific CTLs expanded following vaccination of an individual or test animal with one or more epitopes, wherein said multimeric MHC structure comprises two or more human MHC molecules held together in a single structure by a binding member, said MHC molecules containing an altered α3 domain representing a murine α3 domain

35. A chimeric multimeric MHC structure according to claim 34 wherein said altered α3 domain is a murine α3 domain.

36. A chimeric multimeric MHC structure according to claim 33 or claim 35 further complexed with peptides displaying the epitopes used in the vaccination.

37. A chimeric multimeric MHC structure according to any one of claims 4 to 36 having four human MHC molecules.

38. A chimeric multimeric MHC structure according to any one of claims 34 to 37 wherein the chimeric MHC molecules are fusion proteins comprising human α1 and α2 domains and a murine α3 domain.

Figure 1

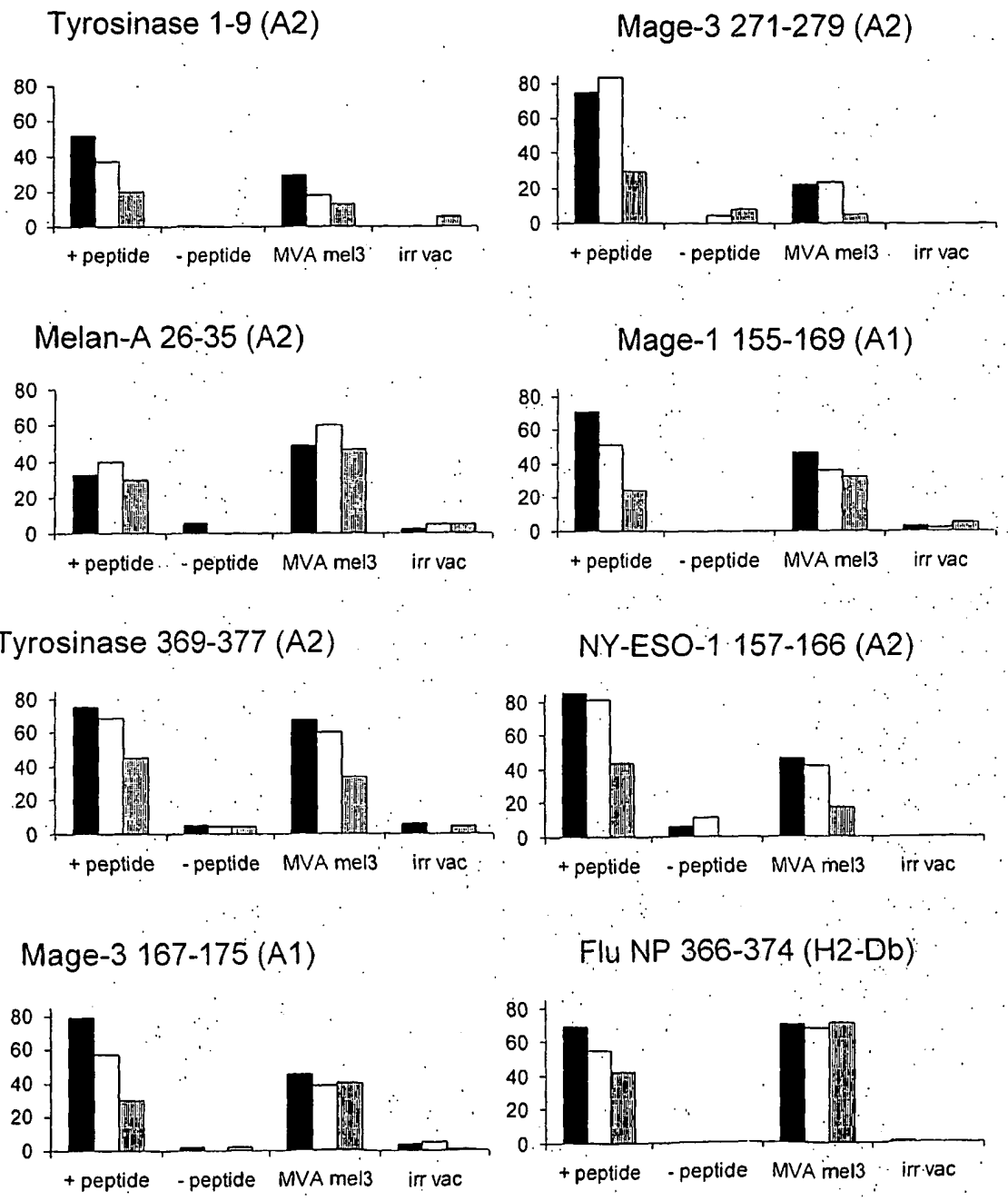

Tyrosinase 1-9 (A2)
Mage-3 271-279 (A2)
Melan-A 26-35 (A2)
Mage-1 155-169 (A1)
Tyrosinase 369-377 (A2)
NY-ESO-1 157-166 (A2)
Mage-3 167-175 (A1)
Flu NP 366-374 (H2-Db)
80
60
40
20
0
+ peptide
- peptide
MVA mel3
irr vac

Figure 2

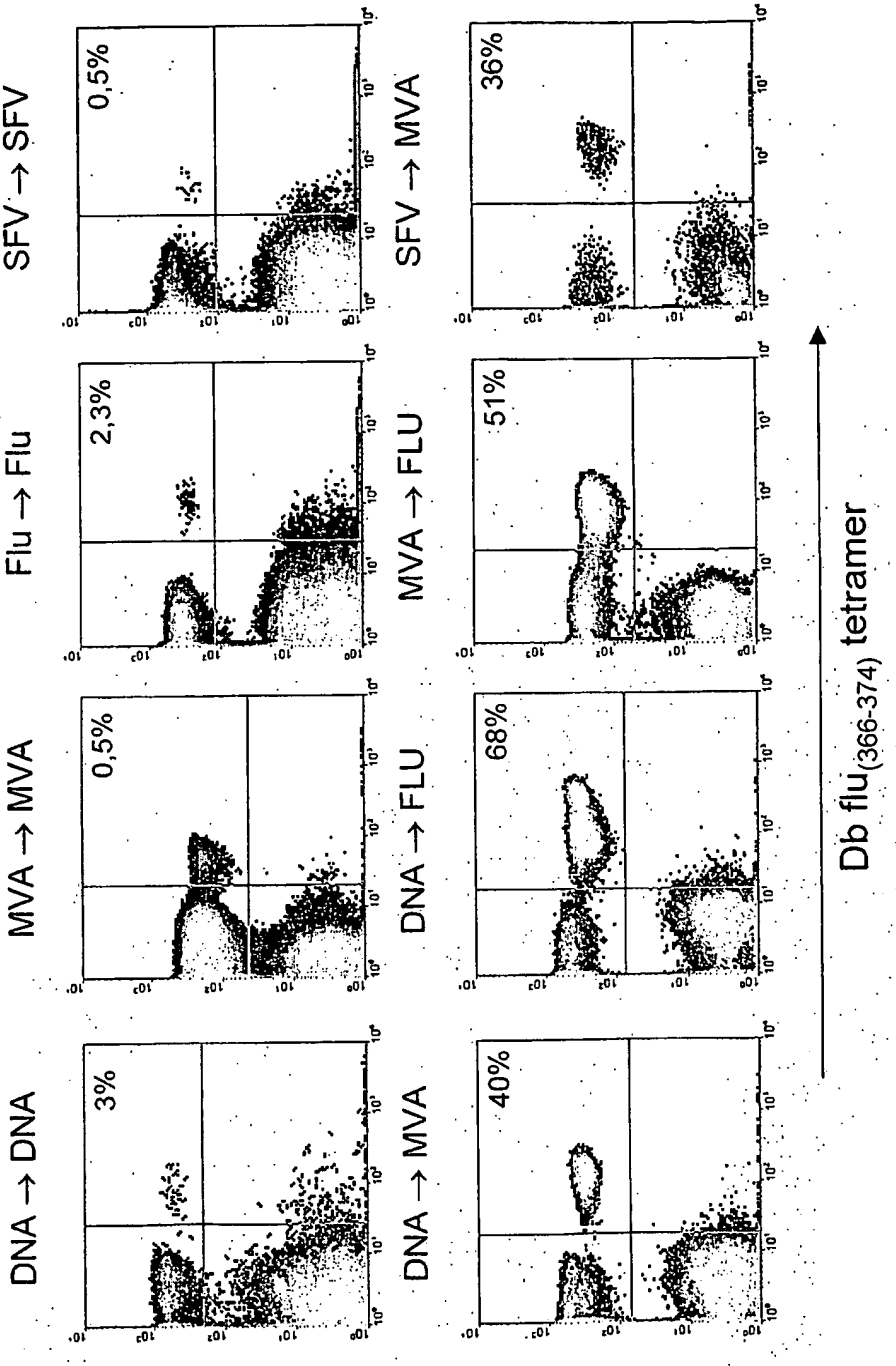

SFV → SFV
0,5%
SFV → MVA
36%
Flu → Flu
2,3%
MVA → FLU
51%
MVA → MVA
0,5%
DNA → FLU
68%
DNA → DNA
3%
DNA → MVA
40%
CD8
Db flu(366-374) tetramer

Figure 3

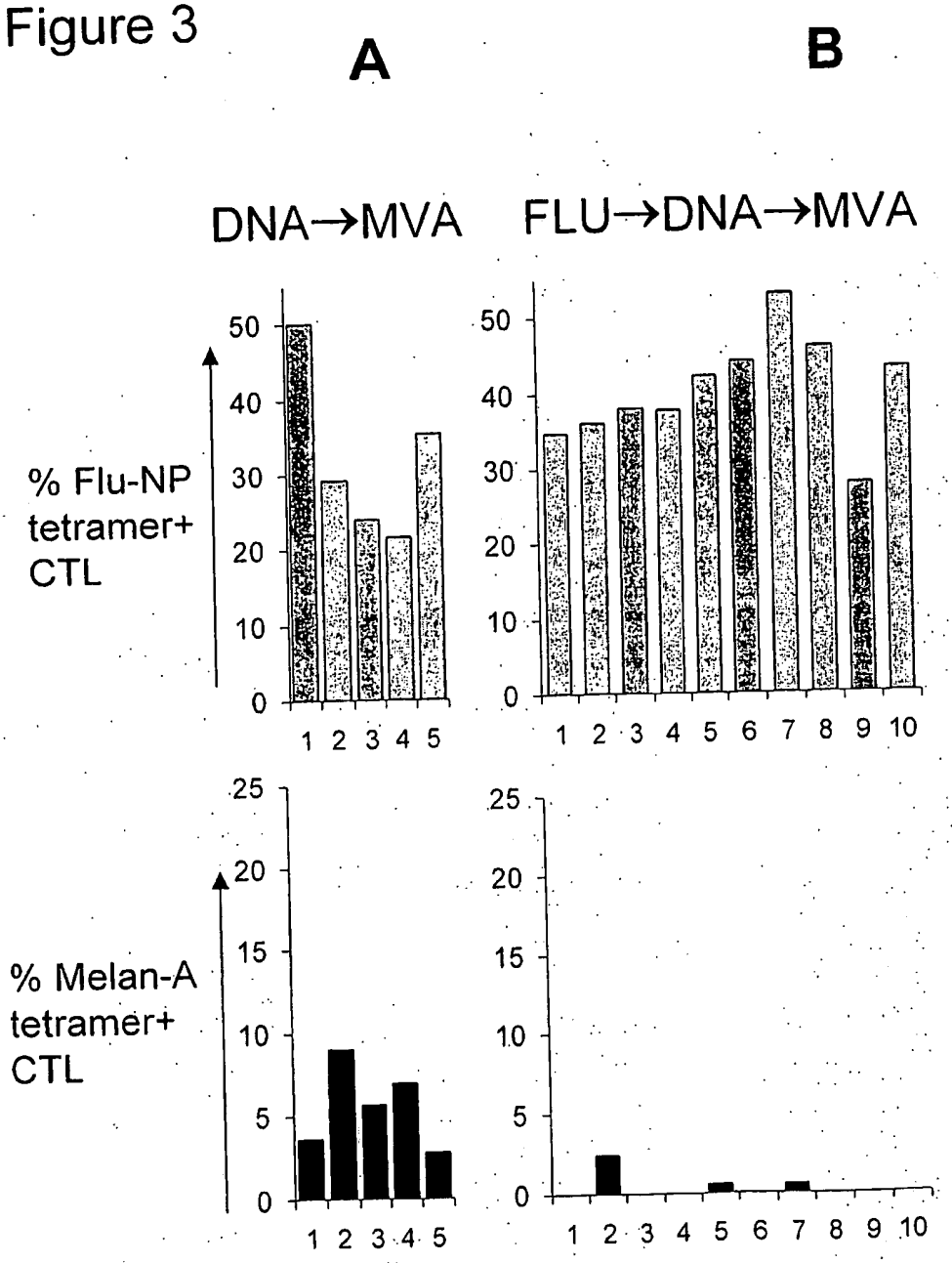

A
B
DNA→MVA
FLU→DNA→MVA
% Flu-NP tetramer+ CTL
% Melan-A tetramer+ CTL
0
10
20
30
40
50
5
15
25
1 2 3 4 5
1 2 3 4 5 6 7 8 9 10

Figure 4

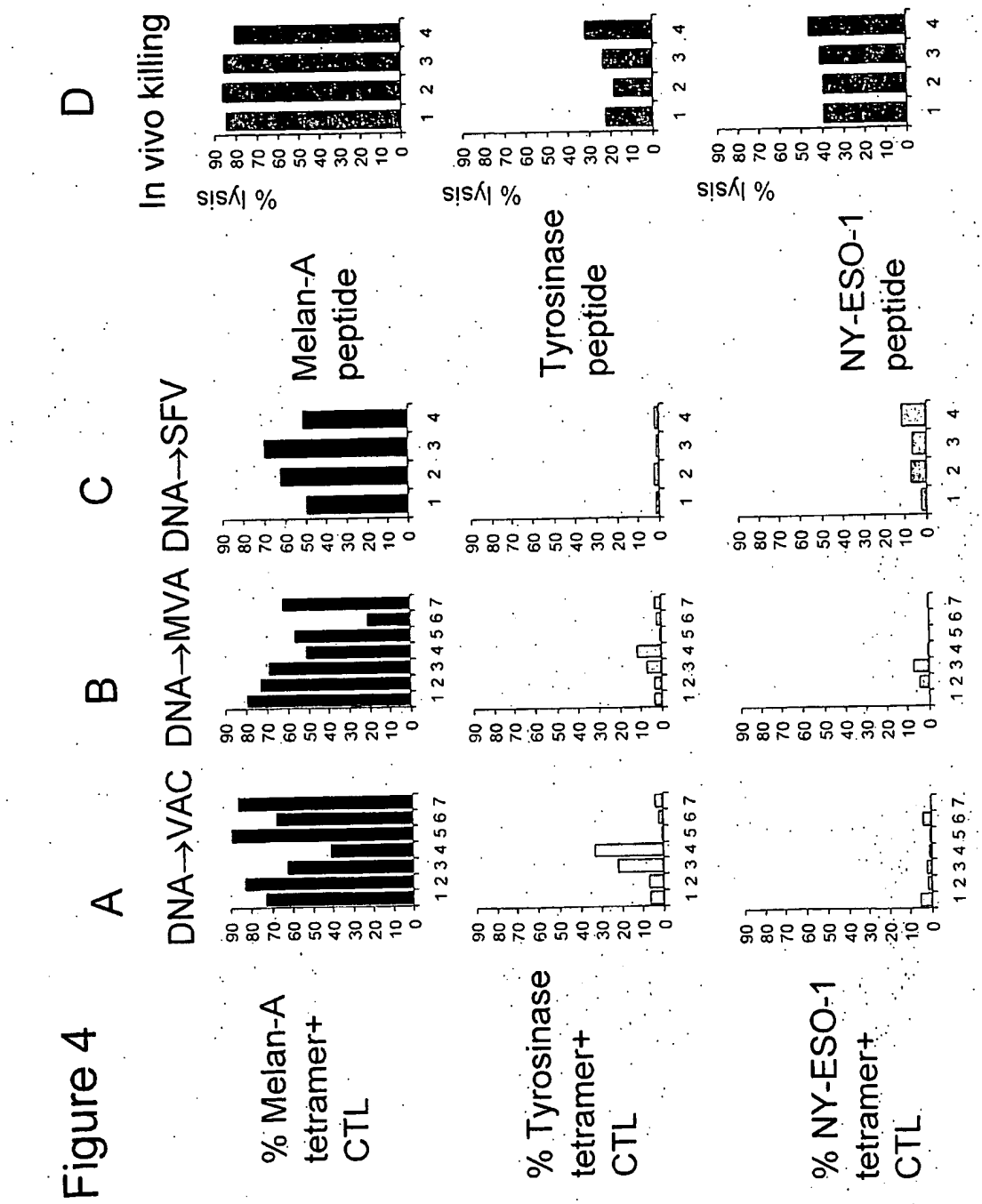

A
B
C
D
DNA→VAC
DNA→MVA
DNA→SFV
In vivo killing
% Melan-A tetramer+ CTL
% Tyrosinase tetramer+ CTL
% NY-ESO-1 tetramer+ CTL
Melan-A peptide
Tyrosinase peptide
NY-ESO-1 peptide
% lysis

Figure 5

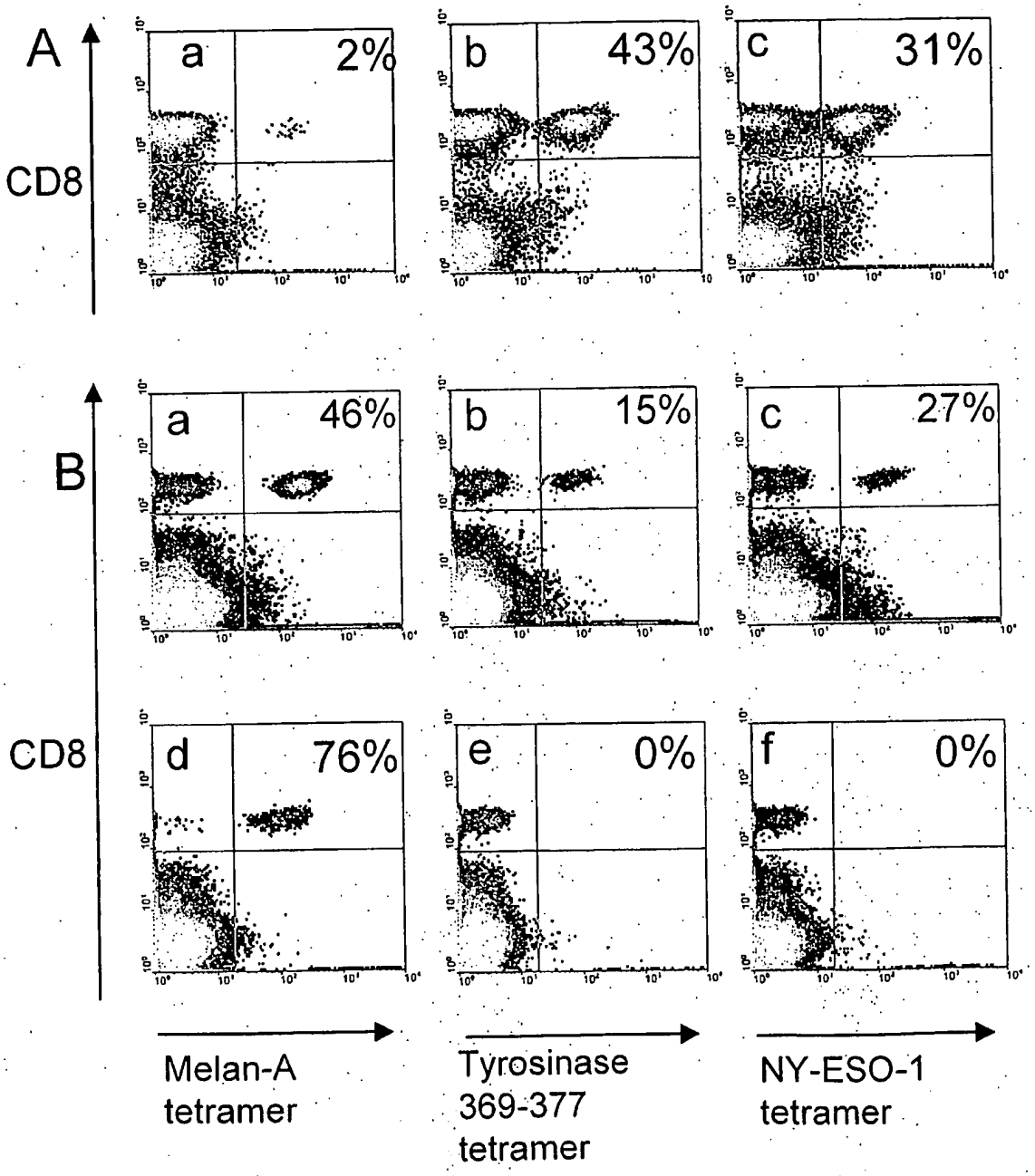

A
CD8
a
2%
b
43%
c
31%
B
CD8
a
46%
b
15%
c
27%
d
76%
e
0%
f
0%
Melan-A tetramer
Tyrosinase 369-377 tetramer
NY-ESO-1 tetramer

Figure 6A

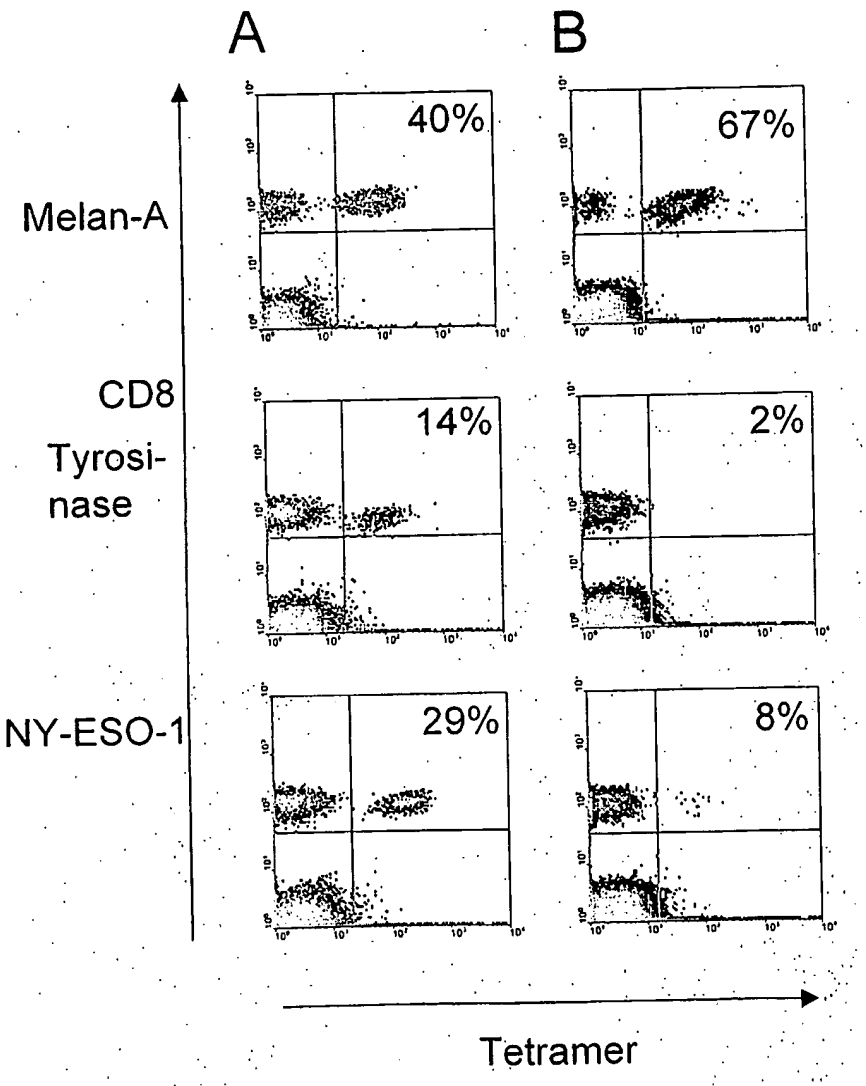


Figure 6B

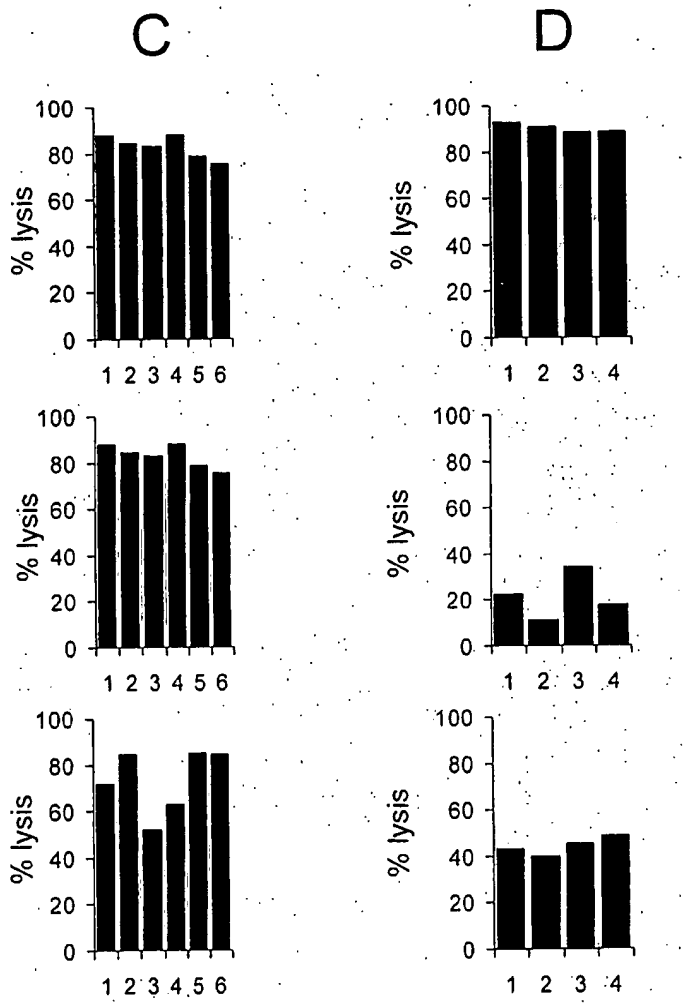
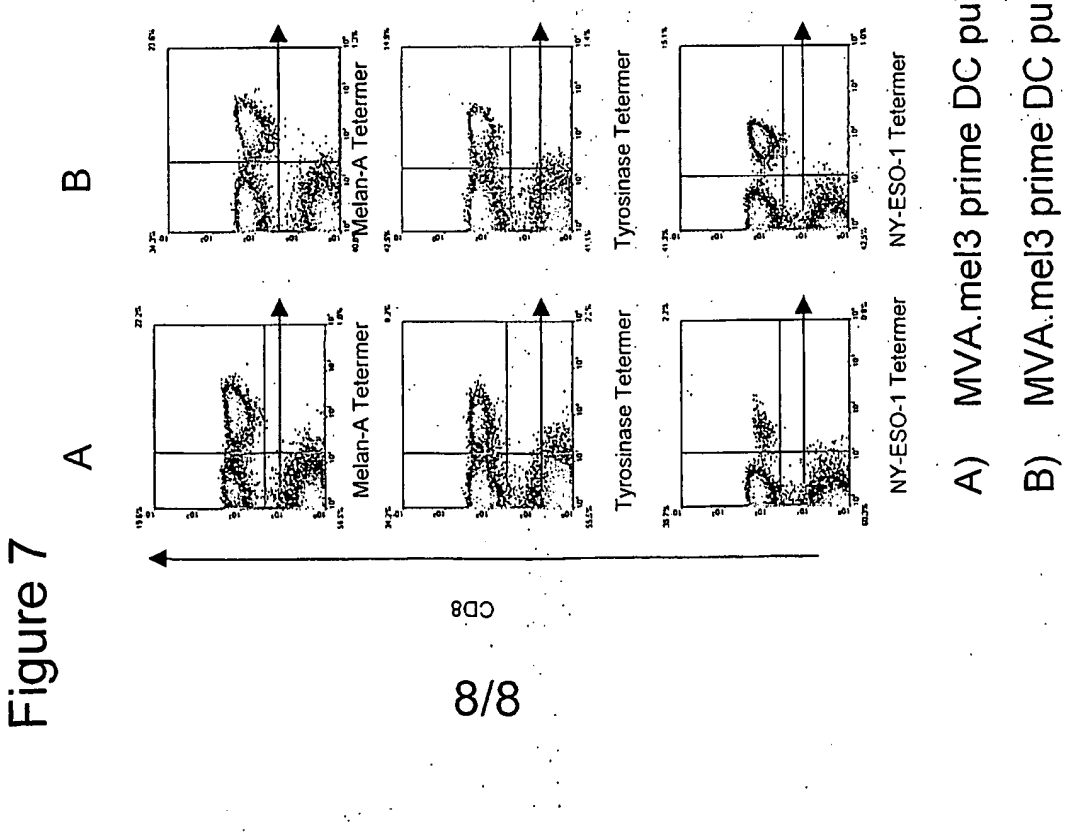


Figure 7



A) MVA.mel3 prime DC pulsed with mixed peptides boost

B) MVA.mel3 prime DC pulsed with single peptides boost